

Amendments to the Claims:

Claim 18 is currently amended.

This amendment adds, changes and/or deletes claims in this application. A detailed listing of all claims that are, or were, in the application, irrespective of whether the claim(s) remain under examination in the application, is presented. The text of all claims presently under examination is presented below in the listing of claims, and all claims are presented with an appropriate defined status identifier.

Detailed and Complete Listing of Claims:

1. (Previously Presented) A method for the expression of a nucleic acid sequence of interest in plant seeds, comprising: (a) preparing a chimeric nucleic acid construct comprising in the 5' to 3' direction of transcription as operably linked components: (1) a seed-specific promoter obtained from flax; and (2) said nucleic acid sequence of interest wherein said nucleic acid of interest is non-native to said seed-specific promoter; (b) introducing said chimeric nucleic acid construct into a plant cell; and (c) growing said plant cell into a mature plant capable of setting seed, wherein said nucleic acid sequence of interest is expressed in the seed under the control of said seed-specific promoter, and wherein said seed-specific promoter comprises a promoter element selected from the group of promoter elements consisting of RY repeat, ABRE, EBOX, and SEF3.
2. (Original) A method according to claim 1 wherein said plant seed is selected from the group of plants consisting of soybean (*Glycine max*), rapeseed (*Brassica napus*, *Brassica campestris*), sunflower (*Helianthus annuus*), cotton (*Gossypium hirsutum*), corn (*Zea mays*), tobacco (*Nicotiana tabacum*), alfalfa (*Medicago sativa*), wheat (*Triticum sp.*), barley (*Hordeum vulgare*), oats (*Avena sativa* L.), sorghum (*Sorghum bicolor*), *Arabidopsis thaliana*, potato (*Solanum sp.*), oil palm (*Eleais guineensis*), groundnut (*Arachis hypogaea*), Brazil nut (*Bertholletia excelsa*) coconut (*Cocus nucifera*), castor (*Ricinus communis*), coriander (*Coriandrum sativum*), squash (*Cucurbita maxima*), jojoba (*Simmondsia chinensis*) and rice (*Oryza sativa*).
3. (Original) A method according to claim 1 wherein said plant seed is flax/linseed (*Linum usitatissimum*).
4. (Original) A method according to claim 1 wherein said plant seed is safflower (*Carthamus tinctorius*).
5. (Canceled).

6. (Original) A method according to claim 1 wherein said seed-specific promoter obtained from flax comprises an RY repeat and an ABRE promoter element.
7. (Original) A method according to claim 6 wherein said RY repeat and ABRE promoter elements are separated from each other by less than 100 nucleotides and more than 20 nucleotides.
8. (Original) A method according to claim 6 wherein said RY repeat and ABRE promoter elements are separated from each other by less than 50 nucleotides and more than 20 nucleotides.
9. (Original) A method according to claim 6 wherein said RY repeat and ABRE promoter elements are separated from each other by less than 35 nucleotides and more than 20 nucleotides.
10. (Original) A method according to claim 6 wherein said seed specific promoter obtained from flax additionally comprises an E-Box promoter element.
11. (Original) A method according to claim 10 wherein said EBOX promoter element is between 250 to 150 nucleotides from the "ATG" start codon.
12. (Original) A method according to claim 10 wherein said EBOX promoter element is between 200 to 175 nucleotides from the "ATG" start codon.
13. (Original) A method according to claim 10 wherein said EBOX promoter element is between 195 to 185 nucleotides from the "ATG" start codon.
14. (Original) A method according to claim 6 wherein said seed-specific promoter obtained from flax additionally comprises an SEF3 promoter element.

15. (Original) A method according to claim 14 wherein said SEF3 promoter element is, between 200 to 50 nucleotides from the "ATG" start codon.

16. (Original) A method according to claim 14 wherein said SEF3 promoter element is between 175 to 100 nucleotides from the "ATG" start codon.

17. (Original) A method according to claim 14 wherein said SEF3 promoter element is between 160 to 145 nucleotides from the "ATG" start codon.

18. (Currently Amended) The method according to claim 1 wherein said flax seed-specific promoter comprises: (a) a nucleic acid sequence as shown in FIG. 1 (SEQ.ID.NO.:1) from nucleotides 1 to 2023, FIG. 2 (SEQ.ID.NO.:4) from nucleotides 1 to 1852, FIG. 3 (SEQ.ID.NO.:6) from nucleotides 1 to 417, or FIG. 4 (SEQ.ID.NO.:8) from nucleotides 1 to 2035, wherein T can also be U; (b) a nucleic acid sequence that is ~~complementary~~ complementary to a nucleic acid sequence of (a); (c) a nucleic acid sequence that has substantial sequence homology to a nucleic acid sequence of (a) or (b); (d) a nucleic acid sequence that is an analog of a nucleic acid sequence of (a), (b) or (c); or (e) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a), (b), (c) or (d) under stringent hybridization conditions.

19. (Previously Presented) Transgenic plant capable of setting seed prepared by a method, comprising: (a) preparing a chimeric nucleic acid construct comprising in the 5' to 3' direction of transcription as operably linked components: (1) a seed-specific promoter obtained from flax; and (2) a nucleic acid sequence of interest wherein said nucleic acid of interest is non-native to said seed-specific promoter; (b) introducing said chimeric nucleic acid construct into a plant cell; and (c) growing said plant cell into a mature plant capable of setting seed, wherein said nucleic acid sequence of interest is expressed in the seed under the control of said seed-specific promoter, and wherein said-specific promoter comprises a promoter element selected from the group of promoter elements consisting of RY repeat, ABRE, EBOX, and SEF3.

20. (Original) A transgenic plant according to claim 19 wherein said plant is selected from the group of plants consisting of soybean (*Glycine max*), rapeseed (*Brassica napus*, *Brassica campestris*), sunflower (*Helianthus annuus*), cotton (*Gossypium hirsutum*), corn (*Zea mays*), tobacco (*Nicotiana tobacum*), alfalfa (*Medicago sativa*), wheat (*Triticum sp.*), barley (*Hordeum vulgare*), oats (*Avena sativa* L.), sorghum (*Sorghum bicolor*), *Arabidopsis thaliana*, potato (*Solanum sp.*), oil palm (*Eleais guineensis*), groundnut (*Arachis hypogaea*), Brazil nut (*Bertholletia excelsa*) coconut (*Cocus nucifera*), castor (*Ricinus communis*), coriander (*Coriandrum sativum*), squash (*Cucurbita maxima*), jojoba (*Simmondsia chinensis*) and rice (*Oryza sativa*).

21. (Original) A transgenic plant according to claim 19 wherein said plant is flax/linseed (*Linum usitatissimum*).

22. (Original) A transgenic plant according to claim 19 wherein said plant is safflower (*Carthamus tinctorius*).

23. (Canceled).

24. (Original) Transgenic plant according to claim 19 wherein said seed-specific promoter obtained from flax comprises an RY repeat and an ABRE promoter element.

25. (Original) Transgenic plant according to claim 19 wherein said RY repeat and ABRE promoter elements are separated from each other by less than 100 nucleotides and more than 20 nucleotides.

26. (Original) Transgenic plant according to claim 25 wherein said RY repeat and ABRE promoter elements are separated from each other by less than 50 nucleotides and more than 20 nucleotides.

27. (Original) Transgenic plant according to claim 25 wherein said RY repeat and ABRE promoter elements are separated from each other by less than 35 nucleotides and more than 20 nucleotides.

28. (Original) Transgenic plant according to claim 25 wherein said seed specific promoter obtained from flax additionally comprises an E-Box promoter element.

29. (Original) Transgenic plant to claim 28 wherein said EBOX promoter element is between 250 to 150 nucleotides from the "ATG" start codon.

30. (Original) Transgenic plant according to claim 28 wherein said EBOX promoter element is between 200 to 175 nucleotides from the "ATG" start codon.

31. (Original) Transgenic plant according to claim 28 wherein said EBOX promoter element is between 195 to 185 nucleotides from the "ATG" start codon.

32. (Original) Transgenic plant according to claim 25 wherein said seed-specific promoter obtained from flax additionally comprises an SEF3 promoter element.

33. (Original) Transgenic plant according to claim 32 wherein said SEF3 promoter element is between 200 to 50 nucleotides from the "ATG" start codon.

34. (Original) Transgenic plant according to claim 32 wherein said SEF3 promoter element is between 175 to 100 nucleotides from the "ATG" start codon.

35. (Original) Transgenic plant according to claim 32 wherein said SEF3 promoter element is between 160 to 145 nucleotides from the "ATG" start codon.

36. (Withdrawn) An isolated nucleic acid sequence capable of directing seed-specific expression in plants and obtained from flax comprising a promoter element selected from the

group of promoter elements consisting of: RY repeat, ABRE, EBOX, SEF3.

37. (Withdrawn) An isolated nucleic acid sequence according to claim 36 wherein said nucleic acid sequence further comprises an RY repeat promoter element and an ABRE promoter element.

38. (Withdrawn) An isolated nucleic acid sequence according to claim 37 wherein said RY repeat promoter element and ABRE promoter element are separated from each other by less than 100 nucleotides and more than 20 nucleotides.

39. (Withdrawn) An isolated nucleic acid sequence according to claim 37 wherein said RY repeat promoter element and ABRE promoter element are separated from each other by less than 50 nucleotides and more than 20 nucleotides.

40. (Withdrawn) An isolated nucleic acid sequence according to claim 37 wherein said RY repeat promoter element and ABRE promoter element are separated from each other by less than 35 nucleotides and more than 20 nucleotides.

41. (Withdrawn) An isolated nucleic acid sequence according to claim 37 additionally comprising an E-Box promoter element.

42. (Withdrawn) An isolated nucleic acid sequence according to claim 41 wherein said EBOX promoter element is between 250 to 150 nucleotides from the "ATG" start codon.

43. (Withdrawn) An isolated nucleic acid sequence according to claim 41 wherein said EBOX promoter element is between 200 to 175 nucleotides from the "ATG" start codon.

44. (Withdrawn) An isolated nucleic acid sequence according to claim 41 wherein said EBOX promoter element is between 195 to 185 nucleotides from the "ATG" start codon.

45. (Withdrawn) An isolated nucleic acid sequence according to claim 37 additionally comprising an SEF3 element.
46. (Withdrawn) An isolated nucleic acid sequence according to claim 45 wherein said SEF3 promoter element is between 200 to 50 nucleotides from the "ATG" start codon.
47. (Withdrawn) An isolated nucleic acid sequence according to claim 45 wherein said SEF3 promoter element is between 175 to 100 nucleotides from the "ATG" start codon.
48. (Withdrawn) An isolated nucleic acid sequence according to claim 45 wherein said SEF3 promoter element is between 160 to 145 nucleotides from the "ATG" start codon.
49. (Withdrawn) An isolated nucleic acid sequence according to claim 36 capable of directing seed-specific expression in a plant comprising: (a) a nucleic acid sequence as shown in FIG. 1 (SEQ.ID.NO.:1), FIG. 2 (SEQ.ID.NO.:4), FIG. 3 (SEQ.ID.NO.:6) or FIG. 4 (SEQ.ID.NO.:8) wherein T can also be U; (b) a nucleic acid sequence that is complementary to a nucleic acid sequence of (a); (c) a nucleic acid sequence that has substantial sequence homology to a nucleic acid sequence of (a) or (b); or (d) a nucleic acid sequence that is an analog of a nucleic acid sequence of (a), (b) or (c); or (e) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a), (b), (c) or (d) under stringent hybridization conditions.
50. (Withdrawn) An isolated chimeric nucleic acid sequence comprising: (a) a first nucleic acid sequence comprising a seed-specific promoter obtained from flax which comprises a nucleic acid sequence comprising a promoter element selected from the group of promoter elements consisting of: RY repeat, ABRE, EBOX, SEF3; and (b) a second nucleic acid sequence non-native to said flax seed-specific promoter.
51. (Withdrawn) An isolated nucleic acid sequence according to claim 48 wherein said nucleic acid sequence further comprises an RY repeat and an ABRE.

52. (Withdrawn) An isolated nucleic acid sequence according to claim 51 wherein said RY repeat and ABRE are separated from each other by less than 100 nucleotides and more than 20 nucleotides.
53. (Withdrawn) An isolated nucleic acid sequence according to claim 51 wherein said RY repeat and ABRE are separated from each other by less than 50 nucleotides and more than 20 nucleotides.
54. (Withdrawn) An isolated nucleic acid sequence according to claim 51 wherein said RY repeat and ABRE are separated from each other by less than 35 nucleotides and more than 20 nucleotides.
55. (Withdrawn) An isolated nucleic acid sequence according to claim 51 additionally comprising an E-Box element.
56. (Withdrawn) An isolated nucleic acid sequence according to claim 55 wherein said EBOX promoter element is between 250 to 150 nucleotides from the "ATG" start codon.
57. (Withdrawn) An isolated nucleic acid sequence according to claim 55 wherein said EBOX promoter element is between 200 to 175 nucleotides from the "ATG" start codon.
58. (Withdrawn) An isolated nucleic acid sequence according to claim 55 wherein said EBOX promoter element is between 195 to 185 nucleotides from the "ATG" start codon.
59. (Withdrawn) An isolated nucleic acid sequence according to claim 51 additionally comprising an SEF3 element.
60. (Withdrawn) An isolated nucleic acid sequence according to claim 59 wherein said SEF3 promoter element is between 200 to 50 nucleotides from the "ATG" start codon.

61. (Withdrawn) An isolated nucleic acid sequence according to claim 59 wherein said SEF3 promoter element is between 175 to 100 nucleotides from the "ATG" start codon.

62. (Withdrawn) An isolated nucleic add sequence according to claim 59 wherein said SEF3 promoter element is between 160 to 145 nucleotides from the "ATG" start codon.

63. (Previously Presented) A method for the expression of a nucleic acid sequence of interest in a plant seed, comprising: (a) introducing the chimeric nucleic add sequence according to claim 50 into a plant cell; and (b) growing said plant cell into a mature plant capable of setting seed, wherein the second nucleic acid sequence is expressed in the seed under the control of the seed specific promoter, and wherein said-specific promoter comprises a promoter element selected from the group of promoter elements consisting of RY repeat, ABRE, EBOX, and SEF3.

64. (Original) A method according to claim 63 wherein said plant cell is selected from the group of plants consisting of soybean (*Glycine max*), rapeseed (*Brassica napus*, *Brassica campestris*), sunflower (*Helianthus annuus*), cotton (*Gossypium hirsutum*), corn (*Zea mays*), tobacco (*Nicotiana tabacum*), alfalafa (*Medicago sativa*), wheat (*Triticum sp.*), barley (*Hordeum vulgare*), oats (*Avena sativa L.*), sorghum (*Sorghum bicolor*), *Arabidopsis thaliana*, potato (*Solanum sp.*), oil palm (*Eleais guineeis*), groundnut (*Arachis hypogaea*), Brazil nut (*Bertholletia excelsa*) coconut (*Cocus nucifera*), castor (*Ricinus communis*), coriander (*Coriandrum sativum*), squash (*Cucurbita maxima*), jojoba (*Simmondsia chinensis*) and rice (*Oryza sativa*).

65. (Original) A method according to claim 63 wherein said plant cell is flax/linseed (*Linum usitatissimum*).

66. (Original) A method according to claim 63 wherein said plant cell is safflower (*Carthamus tinctorius*).

67. (Original) A plant prepared according to the method of claim 63.
68. (Original) A plant cell comprising the chimeric nucleic acid sequence according to claim 50.
69. (Original) Plant seed comprising the chimeric nucleic acid sequence according to claim 50.
70. (Original) Plant seed obtained from a plant prepared according to the method of claim 63.
71. (Original) A recombinant expression vector comprising a nucleic acid sequence according to claim 36.